

## SEQUENCE LISTING

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<120> A NOVEL CAROTENOID HYDROXYLASE GENE AND A METHOD FOR PRODUCING HYDROXY CAROTENOID AND A NOVEL GERANYLGERANYLPYROPHOSPHATE SYNTHETASE GENE

<130> FP-042PCT

<150> JP 2003/388165

<151> 2003-11-26

<150> JP 2004/165919

<151> 2004-06-03

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<170> PatentIn Ver. 2.1

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ctc tat ttc cag ttc tgg gac cgc tgg gcc ggg act gag gtt tgg gcc 11461  
 Leu Tyr Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala  
                   225                  230                  235

gcc ccc tgg cca cca tcc ccg gtc atc cct cca gag cgg ccc tca gcg 11509  
 Ala Pro Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala  
                   240                  245                  250

cct ctt cgg tgatcggctt ggtcaggcgc ggcgtgggcg cccaggccgg 11558  
 Pro Leu Arg  
 255

tcgccatctg cagtatggac gacgaggcca gacgtccccc gccgctcatg gcgatgaccc 11618

gcagggagtc cctcaaatgc cgggtgtcca tgatgaagtt cagcccgtcg cggtcggca 11678

tcagaatgtc caccagcacg gcgtcgggcg accagtcttc gacgatccgc aaccgctcgt 11738

tgaccgttgc tgcggtcagg acttggcaac ccagccgttt cagcatctcc tccagatgaa 11798

gcagaaccag cgaatcgicc tcgatcacgc agactttcac gcccaacctc cagatgcat 11858  
 cagggggaac taacggaiga atcccatgtt gcgtcaactc ggaagacggc gtttccgact 11918  
 ggccatcgcc ttggcgggcg cggtcgtgac cctgcttctg gcggccactg gggtagcgct 11978  
 gcaacgagaa ttc 11991

<210> 3  
 <211> 774  
 <212> DNA  
 <213> Brevundimonas sp.

<220>  
 <221> CDS  
 <222> (1).. (771)

<400> 3  
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 Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile  
 1 5 10 15  
 ggc ctg cgc tat ctg ctg gtc ggc gcg gcg gcc cat ggg ctg ctg tgg 96  
 Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp  
 20 25 30  
 gcc ggg gcg ggc cgg gga cgg gcg ctg aac ctg cgg ccg ccg gcg atg 144  
 Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met  
 35 40 45  
 aag cgc atc cgc gcc gag atc gtc gcc tcc ctg atc gcc tgc ccc atc 192  
 Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile  
 50 55 60  
 tac gcc ctg ccg gcg gcc ctg gtg ctg gag ctg tgg aag cgg ggc ggc 240  
 Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly  
 65 70 75 80  
 acg gcg atc tac agc gat ccc gac gcc tgg ccc ctg tgg tgg ctg ccg 288  
 Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro  
 85 90 95  
 gtc agt ctg atc gtc tat ctg ctg gcg cac gac gcc ttc tac tac tgg 336  
 Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp  
 100 105 110

<210> 4  
<211> 257  
<212> PRT  
<213> Brevundimonas sp.

<400> 4  
Met Leu Arg Asp Leu Leu Ile Thr Thr Leu Ala Leu Ser Leu Ile Ile  
1 5 10 15

Gly Leu Arg Tyr Leu Leu Val Gly Ala Ala Ala His Gly Leu Leu Trp  
                   20                  25                  30

Ala Gly Ala Gly Arg Gly Arg Ala Leu Asn Leu Arg Pro Pro Ala Met  
                   35                  40                  45

Lys Arg Ile Arg Ala Glu Ile Val Ala Ser Leu Ile Ala Cys Pro Ile  
                   50                  55                  60

Tyr Ala Leu Pro Ala Ala Leu Val Leu Glu Leu Trp Lys Arg Gly Gly  
                   65                  70                  75                  80

Thr Ala Ile Tyr Ser Asp Pro Asp Ala Trp Pro Leu Trp Trp Leu Pro  
                   85                  90                  95

Val Ser Leu Ile Val Tyr Leu Leu Ala His Asp Ala Phe Tyr Tyr Trp  
                   100                  105                  110

Val His Arg Ala Leu His His Pro Arg Val Phe Gly Trp Ala His Ala  
                   115                  120                  125

Glu His His Arg Ser Arg Asp Pro Ser Ala Phe Ala Ser Phe Ala Phe  
                   130                  135                  140

Asp Pro Ala Glu Ala Ala Ala Thr Ala Trp Phe Leu Pro Ala Leu Ala  
                   145                  150                  155                  160

Leu Ile Val Pro Ile His Trp Gly Val Ala Leu Thr Leu Leu Thr Leu  
                   165                  170                  175

Met Ser Leu Thr Ala Ala Leu Asn His Ala Gly Arg Glu Val Trp Pro  
                   180                  185                  190

Ala Ala Trp Leu Glu Arg Ala Pro Leu Arg Trp Leu Ile Thr Ala Thr  
                   195                  200                  205

His His Asp Ala His His Lys Arg Phe Asn Gly Asn Tyr Gly Leu Tyr  
                   210                  215                  220

Phe Gln Phe Trp Asp Arg Trp Ala Gly Thr Glu Val Ser Ala Ala Pro  
                   225                  230                  235                  240

Ser Pro Pro Ser Pro Val Ile Pro Pro Glu Arg Pro Ser Ala Pro Leu  
                   245                  250                  255

Arg

<210> 5  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 5  
tacgaattcg atgcccctcg ccctg 25

<210> 6  
<211> 32  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 6  
tagaggatcc tcaaggagtg aactggatcg ta 32

<210> 7  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 7  
tacgaattcg atgaccgccg ccgtcg 26

<210> 8  
<211> 31  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 8

tagaggatcc tcaagactcg ccgcccaca a 31

<210> 9  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 9  
 tacgaattcg ctgtcgcgga tgcaggc 27

<210> 10  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 10  
 tagaggatcc tgcggttcag cagccgataa aa 32

<210> 11  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 11  
 tacgaattcg atgcgagcag cagtgatcgg a 31

<210> 12  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 12

tagaggatcc aagctcttgg agccctgct 29

<210> 13  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 13  
tacgaattcg atgagcgacg ccgtcct 27

<210> 14  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 14  
tagaggatcc tcagatgtgg gtccacagg 29

<210> 15  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 15  
tacgaattcg atgatggcgg tggcgggc 28

<210> 16  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 16



tagaggatcc cccacatctg acggcgct

28

<210> 17

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 17

tacgaattcg atgtccttca tctcttcgg c

31

<210> 18

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 18

tagaggatcc accgccatca tgacgagg

28

<210> 19

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 19

tacgaattcg atggcgatcg tcggcttaa

29

<210> 20

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:primer

<400> 20

tagaggatcc ctagcgtcca agttcggcct 30

<210> 21  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 21  
tacgaattcg atgcccaccc ccgacgacg 29

<210> 22  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 22  
tagaggatcc tcagaagcgg ggctcttcca 30

<210> 23  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 23  
tacgaattcg atggcctggc tgacgtggat 30

<210> 24  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer

<400> 24

tagaggatcc tcaggcgccg ctgctggaa 29

<210> 25  
 <211> 32  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 25  
 tacgaattcg atgttgaggg atctgctcat ca 32

<210> 26  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 26  
 tagaggatcc tcaccgaaga ggcgctgag 29

<210> 27  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 27  
 tacgaattcg atgctgaaac ggctgggtt 29

<210> 28  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:primer

<400> 28

tagaggatcc ctatttccag ttctgggacc g

31

&lt;210&gt; 29

&lt;211&gt; 486

&lt;212&gt; DNA

&lt;213&gt; Brevundimonas sp.

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (483)

&lt;400&gt; 1

atg gcc tgg ctg acg tgg atc gcg ctg ttc ctg acc gcc ttt ttg ggc	48
Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly	
1 5 10 15	
atg gag gcg ttc gcc tgg atc atg cac cgc tat gtg atg cac ggt ttc	96
Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe	
20 25 30	
ctg tgg tcc tgg cac cgc agc cat cat gag ccg cac gat cac ccc ctg	144
Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu	
35 40 45	
gag aag aac gac ctg ttc gcc gtg gtc ttc gcc gcc ccg gcc atc gtc	192
Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val	
50 55 60	
atg gtg gcc gtg ggt ctg cac ctg tgg ccc tgg gcc ctg ccg gtc ggc	240
Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly	
65 70 75 80	
ctg ggg atc acg gcc tat ggg atg gtc tat ttc ttc ttc cac gac ggc	288
Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly	
85 90 95	
ctg gtg cac cgg cgg ttc ccg acg ggc ttt tcc ggg cgg tcc ggc ttc	336
Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe	
100 105 110	
tgg acg cgg cgc atc cag gcg cac cgt ctg cat cac gcc gtg cgc acg	384
Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr	
115 120 125	
cgc gaa ggc tgc gtc tcc ttc ggc ttt ctg tgg gtg cgg tcg gcg cgg	432
Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg	
130 135 140	

gcg ctg aag gcc gaa ctg gct cag aag cgg ggc tct tcc agc agc ggc 480  
 Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly  
 145 150 155 160

gcc tga 486  
 Ala

<210> 30  
 <211> 161  
 <212> PRT  
 <213> Brevundimonas sp.

<400> 30  
 Met Ala Trp Leu Thr Trp Ile Ala Leu Phe Leu Thr Ala Phe Leu Gly  
 1 5 10 15

Met Glu Ala Phe Ala Trp Ile Met His Arg Tyr Val Met His Gly Phe  
 20 25 30

Leu Trp Ser Trp His Arg Ser His His Glu Pro His Asp His Pro Leu  
 35 40 45

Glu Lys Asn Asp Leu Phe Ala Val Val Phe Ala Ala Pro Ala Ile Val  
 50 55 60

Met Val Ala Val Gly Leu His Leu Trp Pro Trp Ala Leu Pro Val Gly  
 65 70 75 80

Leu Gly Ile Thr Ala Tyr Gly Met Val Tyr Phe Phe Phe His Asp Gly  
 85 90 95

Leu Val His Arg Arg Phe Pro Thr Gly Phe Ser Gly Arg Ser Gly Phe  
 100 105 110

Trp Thr Arg Arg Ile Gln Ala His Arg Leu His His Ala Val Arg Thr  
 115 120 125

Arg Glu Gly Cys Val Ser Phe Gly Phe Leu Trp Val Arg Ser Ala Arg  
 130 135 140

Ala Leu Lys Ala Glu Leu Ala Gln Lys Arg Gly Ser Ser Ser Ser Gly  
 145 150 155 160

Ala

<210> 31  
 <211> 897  
 <212> DNA  
 <213> Brevundimonas sp.

<220>  
 <221> CDS  
 <222> (1).. (894)

<400> 31  
 atg gcg atc gtc ggc tta agg ccc cag ccc gtg tcg gac ccc gaa cct 48  
 Met Ala Ile Val Gly Leu Arg Pro Gln Pro Val Ser Asp Pro Glu Pro  
 1 5 10 15  
 cag tcg ccc gag aat ctg cgt ggc ctg gtg cag gac cgg ctg gcc gag 96  
 Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu  
 20 25 30  
 acg gcg ccc tca tcg gac ggt ctt tta gcc ctc gcc gcg cgc gag gcc 144  
 Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala  
 35 40 45  
 ctg ctg gga ccg ggc aag cgg gtc agg ccg gtc gtg gcc atg ttg gcc 192  
 Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala  
 50 55 60  
 gcc gcg cac gtc ggc ggg cgg gcc gag gac gcc ctg gat ttc ggt tgc 240  
 Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys  
 65 70 75 80  
 gcg gtc gaa atg gcc cat gcc gcc tcc ctg gtt ctg gac gac ctg ccc 288  
 Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro  
 85 90 95  
 tgt atg gat gat gcg gcc ttg cgg cgc ggt cag ccg acc ctg cac cgc 336  
 Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg  
 100 105 110  
 cgc cac ggc gag gat gcg gcc gtg ctg gcg gcc gtg gcc ctt ttg aac 384  
 Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn  
 115 120 125  
 caa tcg acc cgg ctg att ctg caa agc cgg gcg ccg tcg gag gcg cgg 432  
 Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg  
 130 135 140  
 ctg ggc gcc ctg gac gat ttg acg cag gcg atc ggc ttc gac ggc ctg 480

Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu  
 145 150 155 160  
 gcc gag ggc cag atg cgc gat ctg cgc gac gat ccc gtt cag cgc gac 528  
 Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp  
 165 170 175  
 gtg gtc gcc ctg cgt cgg atc aac gat ctg aag acc ggc gcc ctg ttc 576  
 Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe  
 180 185 190  
 gtc gcg gcc gcg cgg ggc ggc ggc cgg atg ggc ggc ggc gat gcg gac 624  
 Val Ala Ala Ala Arg Gly Gly Gly Arg Met Gly Gly Gly Asp Ala Asp  
 195 200 205  
 gac ctg gcg cgt ctc gcc gcc ttc ggc gaa gcg gtc ggc ttc gcc ttc 672  
 Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe  
 210 215 220  
 cag ctt tgc gac gac ctg atg gac gcc tgt tgc acg agc gag gcc ttg 720  
 Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu  
 225 230 235 240  
 ggc aag gac gtg ggt cag gat cag ggc gtg acc acc ttc gtg gac ctg 768  
 Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu  
 245 250 255  
 tgg ggc gaa ggc cgg gtc cgc gcc ggg gtg cgc cag tca ctg gcc cgg 816  
 Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg  
 260 265 270  
 gcg gcc gag gcg gtc ggg cac gac agc ccc ctg acg acc tat gtc ctt 864  
 Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu  
 275 280 285  
 cat ctc ttc cgg cag gcc gaa ctt gga cgc tag 897  
 His Leu Phe Arg Gln Ala Glu Leu Gly Arg  
 290 295

<210> 32  
 <211> 298  
 <212> PRT  
 <213> Brevundimonas sp.

<400> 32  
 Met Ala Ile Val Gly Leu Arg Pro Gln Pro Val Ser Asp Pro Glu Pro  
 1 5 10 15

Gln Ser Pro Glu Asn Leu Arg Gly Leu Val Gln Asp Arg Leu Ala Glu  
                   20                  25                  30  
 Thr Ala Pro Ser Ser Asp Gly Leu Leu Ala Leu Ala Ala Arg Glu Ala  
                   35                  40                  45  
 Leu Leu Gly Pro Gly Lys Arg Val Arg Pro Val Val Ala Met Leu Ala  
           50                  55                  60  
 Ala Ala His Val Gly Gly Arg Ala Glu Asp Ala Leu Asp Phe Gly Cys  
           65                  70                  75                  80  
 Ala Val Glu Met Ala His Ala Ala Ser Leu Val Leu Asp Asp Leu Pro  
                   85                  90                  95  
 Cys Met Asp Asp Ala Ala Leu Arg Arg Gly Gln Pro Thr Leu His Arg  
                   100                  105                  110  
 Arg His Gly Glu Asp Ala Ala Val Leu Ala Ala Val Ala Leu Leu Asn  
           115                  120                  125  
 Gln Ser Thr Arg Leu Ile Leu Gln Ser Arg Ala Pro Ser Glu Ala Arg  
           130                  135                  140  
 Leu Gly Ala Leu Asp Asp Leu Thr Gln Ala Ile Gly Phe Asp Gly Leu  
           145                  150                  155                  160  
 Ala Glu Gly Gln Met Arg Asp Leu Arg Asp Asp Pro Val Gln Arg Asp  
                   165                  170                  175  
 Val Val Ala Leu Arg Arg Ile Asn Asp Leu Lys Thr Gly Ala Leu Phe  
                   180                  185                  190  
 Val Ala Ala Ala Arg Gly Gly Gly Arg Met Gly Gly Gly Asp Ala Asp  
           195                  200                  205  
 Asp Leu Ala Arg Leu Ala Ala Phe Gly Glu Ala Val Gly Phe Ala Phe  
           210                  215                  220  
 Gln Leu Cys Asp Asp Leu Met Asp Ala Cys Ser Thr Ser Glu Ala Leu  
           225                  230                  235                  240  
 Gly Lys Asp Val Gly Gln Asp Gln Gly Val Thr Thr Phe Val Asp Leu  
                   245                  250                  255  
 Trp Gly Glu Gly Arg Val Arg Ala Gly Val Arg Gln Ser Leu Ala Arg  
           260                  265                  270



Ala Ala Glu Ala Val Gly His Asp Ser Pro Leu Thr Thr Tyr Val Leu  
275 280 285

His Leu Phe Arg Gln Ala Glu Leu Gly Arg  
290 295